G. Bagaisky



1653

pt#13



RAW SEQUENCE LISTING DATE: 01/08/2001
PATENT APPLICATION: US/09/403,861A TIME: 15:12:03

Input Set : A:\Riccardi1.txt
Output Set: N:\CRF3\01082001\I403861A.raw

SEQUENCE LISTING

(1) GENERAL INFORMATION:
(i) APPLICANT: RICCARDI, Carlo
(ii) TITLE OF INVENTION: INTRACELLULAR MODULATORS OF APOPTIC CELL DEATH PATHWAYS
(iii) NUMBER OF SEQUENCES: 15
(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
(B) STREET: 624 Ninth Street, N.W., Suite 300
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20001
(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
(vi) CURRENT APPLICATION DATA:
C--> (A) APPLICATION NUMBER: US/09/403,861A
C--> (B) FILING DATE: 11-Feb-2000
C--> (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/EP98/02490
(B) FILING DATE: 27-APR-1998
(A) APPLICATION NUMBER: EP 97107033.9
(B) FILING DATE: 28-APR-1997
(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: YUN, Allen C.
(B) REGISTRATION NUMBER: 37,971
(C) REFERENCE/DOCKET NUMBER: RICCARDI=1
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 202-628-5197
(B) TELEFAX: 202-737-3528
(2) INFORMATION FOR SEQ ID NO: 1:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1972 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(ix) FEATURE:
(A) NAME/KEY: CDS
C--> (B) LOCATION:206..616
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
CTGGCTGCTG TGGAGTTTGT GACATACTAG GTGACACCCT TGGAGTCACT TCTCTTCAAC 60

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Input Set : A:\Riccardil.txt
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71 TCCAGCTTAG AAGTGCCTGC CTGGCTCAGG GTCTGCACTG CAGCCTACTC CTTGCTTCAG      120
73 GGCCTGACTG CAACCCCAAA GCCTATCCTA TAGCGGCAGC GCCAGCAGCC ACTCAAACCA      180
75 GCCACAGCTC CCCGGCAACC GAACC ATG AAC ACC GAA ATG TAT CAG ACC CCC        232
76                            Met Asn Thr Glu Met Tyr Gln Thr Pro
77                              1               5
79 ATG GAG GTG GCC GTC TAT CAG CTG CAC AAT TTC TCC ACC TCC TTC TTT        280
80 Met Glu Val Ala Val Tyr Gln Leu His Asn Phe Ser Thr Ser Phe Phe
81  10                  15                  20                  25
83 TCT TCT CTG CTT GGA GGG GAT GTG GTT TCC GTT AAA CTG GAT AAC AGT        328
84 Ser Ser Leu Leu Gly Gly Asp Val Val Ser Val Lys Leu Asp Asn Ser
85                  30                  35                  40
87 GCC TCC GGA GCC AGT GTG GTG GCC CTA GAC AAC AAG ATT GAG CAG GCC        376
88 Ala Ser Gly Ala Ser Val Val Ala Leu Asp Asn Lys Ile Glu Gln Ala
89              45                  50                  55
91 ATG GAC CTC GTG AAG AAC CAC CTG ATG TAC GCT GTG AGA GAG GAG GTG        424
92 Met Asp Leu Val Lys Asn His Leu Met Tyr Ala Val Arg Glu Glu Val
93          60                  65                  70
95 GAG GTC CTA AAG GAG CAG ATT CGT GAG CTG CTT GAG AAG AAC TCC CAG        472
96 Glu Val Leu Lys Glu Gln Ile Arg Glu Leu Leu Glu Lys Asn Ser Gln
97      75                  80                  85
99 CTG GAG CGC GAG AAC ACC CTC CTG AAG ACG CTG GCA AGC CCC GAG CAA        520
100 Leu Glu Arg Glu Asn Thr Leu Leu Lys Thr Leu Ala Ser Pro Glu Gln
101  90                  95                 100                 105
103 CTG GAA AAG TTC CAG TCC CGG CTG AGC CCT GAA GAG CCA GCA CCT GAA       568
104 Leu Glu Lys Phe Gln Ser Arg Leu Ser Pro Glu Glu Pro Ala Pro Glu
105                 110                 115                 120
107 GCC CCA GAA ACC CCG GAA ACC CCG GAA GCC CCT GGT GGT TCT GCG GTG       616
108 Ala Pro Glu Thr Pro Glu Thr Pro Glu Ala Pro Gly Gly Ser Ala Val
109             125                 130                 135
111 TAAGTGGCTC TGTCCTTAGG GTGGGCAGAG CCACATCTTG TTCTACCTAG TTCTTTCCAG      676
113 TTTGTTTTTG GCTCCCCAAG GGTCATCTCA TGTGGAGAAC TTTACACCTA ACATAGCTGG      736
115 TGCCAAGAGA TGTCCCAAGG ACATGCCCAT CTGGGTCCAC TCCAGTGACA GACCCCTGAC      796
117 AAAGAGCAGG TCTCTGGAGA CTAAGTTGCA TGGGGCCTAG TAACACCAAG CCAGTGAGCC      856
119 TGTCGTGTCA CCGGGCCCTG GGGGCTCCCA GGGCTGGGCA ACTTAGTTAC AGCTGACCAA      916
121 GGAGAAAGTA GTTTTGAGAT GTGATGCCAG TGTGCTCCAG AAAGTGTAAG GGGTCTGTTT      976
123 TTCATTTCCA TGGACATCTT CCACAGCTTC ACCTGACAAT GACTGTTCCT ATGAAGAAGC     1036
125 CACTTGTGTT CTAAGCAGAA GCAACCTCTC TCTTCTTCCT CTGTCTTTTC CAGGCAGGGG     1096
127 CAGAGATGGG AGAGATTGAG CCAAATGAGC CTTCTGTTGG TTAATACTGT ATAATGCATG     1156
129 GCTTTGTGCA CAGCCCAGTG TGGGGTTACA GCTTTGGGAT GACTGCTTAT AAAGTTCTGT     1216
131 TTGGTTAGTA TTGGCATCGT TTTTCTATAT AGCCATAATG CGTATATATA CCCATAGGGC     1276
133 TAGATCTATA TCTTAGGGTA GTGATGTATA CATATACACA TACACCTACA TGTTGAAGGG     1336
135 CCTAACCAGC TTTGGGAGTA CTGACTGGTC TCTTATCTCT TAAAGCTAAG TTTTTCACTG     1396
137 TGCTAATTTA CCAAATTGAT CCAGTTTGTC CTTTAGATTA AATAAGACTC GATATGAGGG     1456
139 AGGGAGGGGA AGACCAGCCT CACAATGCGG CCACAGATGC CTTGCTGCTG CAGTCCTCCC     1516
141 TGATCTGTCC ACTGAAGACA TGAAGTCCTC TTTTGAATGC CAAACCCACC ATTCATTGGT     1576
143 GCTGACTACA TAGAATGGGG TTGAGAGAAG ATCAGTTTGG ACTTCACATT TTTGTTTTAA     1636
145 GTTTTAGGTT GTTTTTTTTT GGTTTTGTTT GTTTGTTTGT TTGTTTGTTT TTGTTTTTTG     1696
147 TTTTTCTTTT TTAAGTTCTT GTGGGGAAAC TTTGGGGTTA ATCAAAGGAT GTAGTCCTGT     1756
149 GGTAGACCAG AGGAGTAACT AGTTTTGATC CTTTGGGGTG TGGAAAATGT ACCCAGGAAG     1816
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151 CTTGTGTAAG GAGGTTCTGT GACAGTGAAC ACTTTCCACT TTCTGACACC TCATCCTGCT    1876
153 GTACGACTCC AGGATTTGGA TTTCGATTTT TCAAATGTAG CTTGAAATTT CAATAAACTT    1936
155 TGCTCCTTTT TCTAAAAATA AAAAAAAAAA AAAAAA                             1972
158 (2) INFORMATION FOR SEQ ID NO: 2:
160      (i) SEQUENCE CHARACTERISTICS:
161           (A) LENGTH: 137 amino acids
162           (B) TYPE: amino acid
163           (D) TOPOLOGY: linear
165     (ii) MOLECULE TYPE: protein
167     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
169 Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
170   1               5                  10                  15
172 Leu His Asn Phe Ser Thr Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
173              20                  25                  30
175 Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
176          35                  40                  45
178 Ala Leu Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
179      50                  55                  60
181 Leu Met Tyr Ala Val Arg Glu Glu Val Glu Val Leu Lys Glu Gln Ile
182  65                  70                  75                  80
184 Arg Glu Leu Leu Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
185                 85                  90                  95
187 Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Arg
188             100                 105                 110
190 Leu Ser Pro Glu Glu Pro Ala Pro Glu Ala Pro Glu Thr Pro Glu Thr
191         115                 120                 125
193 Pro Glu Ala Pro Gly Gly Ser Ala Val
194     130                 135
196 (2) INFORMATION FOR SEQ ID NO: 3:
198      (i) SEQUENCE CHARACTERISTICS:
199           (A) LENGTH: 20 base pairs
200           (B) TYPE: nucleic acid
201           (C) STRANDEDNESS: single
202           (D) TOPOLOGY: linear
204     (ii) MOLECULE TYPE: cDNA
206    (iii) HYPOTHETICAL: NO
208     (iv) ANTI-SENSE: NO
210     (ix) FEATURE:
211           (A) NAME/KEY: misc_feature
212           (B) LOCATION:1..20
213           (D) OTHER INFORMATION:/note= "PCR forward primer"
215     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
217 CCATCTGGGT CCACTCCAGT                                               20
219 (2) INFORMATION FOR SEQ ID NO: 4:
221      (i) SEQUENCE CHARACTERISTICS:
222           (A) LENGTH: 20 base pairs
223           (B) TYPE: nucleic acid
224           (C) STRANDEDNESS: single
225           (D) TOPOLOGY: linear
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PATENT APPLICATION: US/09/403,861A TIME: 15:12:03

Input Set : A:\Riccardil.txt
Output Set: N:\CRF3\01082001\I403861A.raw

(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION:1..20
(D) OTHER INFORMATION:/note= "PCR reverse primer"
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
AGGACAGTGG GAGTGGCACC 20

(2) INFORMATION FOR SEQ ID NO: 5:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1946 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION:241..642
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

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AATTCGGGGG CCGTGGAGTT TGTGACATAC GAGGTGACAC CCCTCGAGTC ACTTCCCTTC      60
AACTCCAGCT GGAGCGCCTG CTTGGCTTTG GGTTCGTTCT GCAGCCTTCG CCCCGCTCCT     120
AGCCTCAGGG CCGGACTCCA GCGCAGAGCC CAGCCCAGCG CAGCCTGCCA GCAGCCACCC     180
AGCCGCCCAG CCGCCCAGCC CCGCACGAAA CCCGGCCAGA GCTTCCTAGC AGCCCGAGCC     240
ATG AAC ACC GAA ATG TAT CAG ACC CCC ATG GAG GTG GCG GTC TAC CAG       288
Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
W--> 270                  5                  10                  15
CTG CAC AAT TTC TCC ATC TCC TTC TTC TCT TCT CTG CTT GGA GGG GAT       336
Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
274              20                  25                  30
GTG GTT TCC GTT AAG CTG GAC AAC AGT GCC TCC GGA GCC AGC GTG GTG       384
Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
278          35                  40                  45
GCC ATA GAC AAC AAG ATC GAA CAG GCC ATG GAT CTG GTG AAG AAT CAT       432
Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
282      50                  55                  60
CTG ATG TAT GCT GTG AGA GAG GAG GTG GAG ATC CTG AAG GAG CAG ATC       480
Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile
286  65                  70                  75                  80
CGA GAG CTG GTG GAG AAG AAC TCC CAG CTA GAG CGT GAG AAC ACC CTG       528
Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
290                  85                  90                  95
TTG AAG ACC CTG GCA AGC CCA GAG CAG CTG GAG AAG TTC CAG TCC TGT       576
Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys
294              100                 105                 110
CTG AGC CCT GAA GAG CCA GCT CCC GAA TCC CCA CAA GTG CCC GAG GCC       624
Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala
298          115                 120                 125
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300 CCT GGT GGT TCT GCG GTG TAAGTGGCTC TGTCCTCAGG GTGGGCAGAG              672
301 Pro Gly Gly Ser Ala Val
302     130
304 CCACTAAACT TGTTTTACCT AGTTCTTTCC AGTTTGTTTT TGGCTCCCCA AGCATCATCT      732
306 CACGAGGAGA ACTTTACACC TAGCACAGCT GGTGCCAAGA GATGTCCTAA GGACATGGCC      792
308 ACCTGGGTCC ACTCCAGCGA CAGACCCCTG ACAAGAGCAG GTCTCTGGAG GCTGAGTTGC      852
310 ATGGGGCCTA GTAACACCAA GCCAGTGAGC CTCTAATGCT ACTGCGCCCT GGGGGCTCCC      912
312 AGGGCCTGGG CAACTTAGCT GCAACTGGCA AAGGAGAAGG GTAGTTTGAG GTGTGACACC      972
314 AGTTTGCTCC AGAAAGTTTA AGGGGTCTGT TTCTCATCTC CATGGACATC TTCAACAGCT     1032
316 TCACCTGACA ACGACTGTTC CTATGAAGAA GCCACTTGTG TTTTAAGCAG AGGCAACCTC     1092
318 TCTCTTCTCC TCTGTTTCGT GAAGGCAGGG GACACAGATG GGAGAGATTG AGCCAAGTCA     1152
320 GCCTTCTGTT GGTTAATATG GTATAATGCA TGGCTTTGTG CACAGCCCAG TGTGGGATTA     1212
322 CAGCTTTGGG ATGACCGCTT ACAAAGTTCT GTTTGGTTAG TATTGGCATA GTTTTTCTAT     1272
324 ATAGCCATAA ATGCGTATAT ATACCCATAG GGCTAGATCT GTATCTTAGT GTAGCGATGT     1332
326 ATACATATAC ACATCCACCT ACATGTTGAA GGGCCTAACG AGCCTTGGGA GTATTGACTG     1392
328 GTCCCTTACC TCTTATGGCT AAGTCTTTGA CTGTGTTCAT TTACCAAGTT GACCCAGTTT     1452
330 GTCTTTTAGG TTAAGTAAGA ACTCGAGAGT AAAGGCAAGG AGGGGGGCCA GCCTCTGAAT     1512
332 GCGGCCACGG ATGCCTTGCT GCTGCAACCC TTTCCCCAGC TGTCCACTGA AACGTGAAGT     1572
334 CCTGTTTTGA ATGCCAAACC CACCATTCAC TGGTGCTGAC TACATAGAAT GGGTTGAGAG     1632
336 AAGATCAGTT TGGGCTTCAC AGTGTCATTT GAAAAAGCGT TTTTGTTTTG TTTTGAATTA     1692
338 TTGTGGAAAA CTTTCAAGTG AACAGAAGGA TGGTGTCCTA CTGTGGATGA GGGATGAACA     1752
340 AGGGGATGGC TTTGATCCAA TGGAGCCTGG GAGGTGTGCC CAGAAAGCTT GTCTGTAGCG     1812
342 GGTTTTGTGA GAGTGAACAC TTTCCACTTT TTGACACCTT ATCCTGATGT ATGGTTCCAG     1872
344 GATTTGGATT TTGATTTTCC AAATGTAGCT TGAAATTTCA ATAAACTTTG CTCTGTTTTT     1932
346 CTAAAAAATA AAAA                                                      1946
349 (2) INFORMATION FOR SEQ ID NO: 6:
351      (i) SEQUENCE CHARACTERISTICS:
352           (A) LENGTH: 134 amino acids
353           (B) TYPE: amino acid
354           (D) TOPOLOGY: linear
356     (ii) MOLECULE TYPE: protein
358     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
360 Met Asn Thr Glu Met Tyr Gln Thr Pro Met Glu Val Ala Val Tyr Gln
361   1               5                  10                  15
363 Leu His Asn Phe Ser Ile Ser Phe Phe Ser Ser Leu Leu Gly Gly Asp
364              20                  25                  30
366 Val Val Ser Val Lys Leu Asp Asn Ser Ala Ser Gly Ala Ser Val Val
367          35                  40                  45
369 Ala Ile Asp Asn Lys Ile Glu Gln Ala Met Asp Leu Val Lys Asn His
370      50                  55                  60
372 Leu Met Tyr Ala Val Arg Glu Glu Val Glu Ile Leu Lys Glu Gln Ile
373  65                  70                  75                  80
375 Arg Glu Leu Val Glu Lys Asn Ser Gln Leu Glu Arg Glu Asn Thr Leu
376                  85                  90                  95
378 Leu Lys Thr Leu Ala Ser Pro Glu Gln Leu Glu Lys Phe Gln Ser Cys
379             100                 105                 110
381 Leu Ser Pro Glu Glu Pro Ala Pro Glu Ser Pro Gln Val Pro Glu Ala
382         115                 120                 125
384 Pro Gly Gly Ser Ala Val
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VERIFICATION SUMMARY DATE: 01/08/2001
PATENT APPLICATION: US/09/403,861A TIME: 15:12:04

Input Set : A:\Riccardil.txt
Output Set: N:\CRF3\01082001\I403861A.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:270 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:394 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=7, Value=[pepetide]